

1633

RAW SEQUENCE LISTING DATE: 05/16/2000
 PATENT APPLICATION: US/09/230,048 TIME: 06:46:19

Input Set : A:\Pdg-127.app
 Output Set: N:\CRF3\05162000\I230048.raw

ENTERED

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4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: FLECKENSTEIN, Bernhard
7               ALBRECHT, Jens-Christian
8               NEIPEL, Frank
9               FRIEDMAN-KIEN, Alvin
10              HUANG, Yao-Qi
12   (ii) TITLE OF INVENTION: VIRAL INTERLEUKIN-6
14   (iii) NUMBER OF SEQUENCES: 4
16   (iv) CORRESPONDENCE ADDRESS:
17       (A) ADDRESSEE: FOLEY & LARDNER
18       (B) STREET: 3000 K Street, N.W.
19       (C) CITY: Washington
20       (D) STATE: D.C.
21       (E) COUNTRY: U.S.A.
22       (F) ZIP: 20007-5109
24   (v) COMPUTER READABLE FORM:
25       (A) MEDIUM TYPE: Floppy disk
26       (B) COMPUTER: IBM PC compatible
27       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
C--> 30   (vi) CURRENT APPLICATION DATA:
C--> 31       (A) APPLICATION NUMBER: US/09/230,048
C--> 32       (B) FILING DATE: 12-Mar-1999
33       (C) CLASSIFICATION:
35   (vii) PRIOR APPLICATION DATA:
36       (A) APPLICATION NUMBER: WO PCT/EP96/03199
37       (B) FILING DATE: 19-JUL-1996
39   (viii) ATTORNEY/AGENT INFORMATION:
40       (A) NAME: Granados, Patricia D.
41       (B) REGISTRATION NUMBER: 33,683
42       (C) REFERENCE/DOCKET NUMBER: 058315/0129
44   (ix) TELECOMMUNICATION INFORMATION:
45       (A) TELEPHONE: (202) 672-5300
46       (B) TELEFAX: (202) 672-5399
49 (2) INFORMATION FOR SEQ ID NO: 1:
51   (i) SEQUENCE CHARACTERISTICS:
52       (A) LENGTH: 612 base pairs
53       (B) TYPE: nucleic acid
54       (C) STRANDEDNESS: double
55       (D) TOPOLOGY: linear
57   (ii) MOLECULE TYPE: DNA (genomic)
60   (ix) FEATURE:
61       (A) NAME/KEY: CDS
62       (B) LOCATION: 1..612
65   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG CTG
68 Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu

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RAW SEQUENCE LISTING

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69      1          5          10          15
71 GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT GAA AAG      96
72 Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
73      20          25          30
75 GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG ATC GAT GAA      144
76 Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
77      35          40          45
79 TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC AAG GGT ATT CTA      192
80 Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
81      50          55          60
83 GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA GCC ATC AAC GAT ACT      240
84 Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
85      65          70          75          80
87 GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG ACT AGC TGC CTT AAA AAG      288
88 Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
89      85          90          95
91 CTC GCC GAT GGC TTT TTT GAA TTC GAG GTG TTG TTT AAG TTT TTA ACG      336
92 Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
93      100          105          110
95 ACG GAG TTT GGA AAA TCA GTG ATA AAC GTG GAC GTC ATG GAG CTT CTG      384
96 Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
97      115          120          125
99 ACG AAG ACC TTA GGA TGG GAC ATA CAG GAA GAG CTC AAT AAG CTG ACT      432
100 Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
101      130          135          140
103 AAG ACG CAC TAC AGT CCA CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG      480
104 Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
105      145          150          155          160
107 CTT CAG GGA CTT AAG TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT      528
108 Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
109      165          170          175
111 CTG AGT GCA ATG GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC      576
112 Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
113      180          185          190
115 TCT ATC CCA GAC GTG ACT CCT GAC GTC CAC GAT AAG      612
116 Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
117      195          200
120 (2) INFORMATION FOR SEQ ID NO: 2:
121 (i) SEQUENCE CHARACTERISTICS:
122 (A) LENGTH: 204 amino acids
123 (B) TYPE: amino acid
124 (D) TOPOLOGY: linear
125 (ii) MOLECULE TYPE: protein
126 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
131 Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Val Gly Ser Leu Leu
132      1          5          10          15
134 Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
135      20          25          30
137 Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu

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138          35          40          45
140 Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
141          50          55          60
143 Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
144 65          70          75          80
146 Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
147          85          90          95
149 Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
150          100          105          110
152 Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
153          115          120          125
155 Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
156          130          135          140
158 Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
159 145          150          155          160
161 Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
162          165          170          175
164 Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
165          180          185          190
167 Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
168          195          200
170 (2) INFORMATION FOR SEQ ID NO: 3:
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 212 amino acids
174 (B) TYPE: amino acid
175 (C) STRANDEDNESS:
176 (D) TOPOLOGY: linear
178 (ii) MOLECULE TYPE: protein
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
185 Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
186 1 5 10 15
188 Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
189 20 25 30
191 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
192 35 40 45
194 Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
195 50 55 60
197 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
198 65 70 75 80
200 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
201 85 90 95
203 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
204 100 105 110
206 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
207 115 120 125
209 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
210 130 135 140
212 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
213 145 150 155 160

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215   Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
216                               165          170          175
218   Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
219                               180          185          190
221   Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
222                               195          200          205
224   Leu Arg Gln Met
225                               210
227 (2) INFORMATION FOR SEQ ID NO: 4:
229   (i) SEQUENCE CHARACTERISTICS:
230       (A) LENGTH: 211 amino acids
231       (B) TYPE: amino acid
232       (C) STRANDEDNESS:
233       (D) TOPOLOGY: linear
235   (ii) MOLECULE TYPE: protein
240   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
242   Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly
243       1           5           10           15
245   Leu Met Leu Val Thr Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg
246       20           25           30
248   Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr
249       35           40           45
251   Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu
252       50           55           60
254   Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp
255       65           70           75           80
257   Asp Ala Leu Ala Glu Asn Asn Leu Lys Leu Pro Glu Ile Gln Arg Asn
258       85           90           95
260   Asp Gly Cys Tyr Gln Thr Gly Tyr Asn Gln Glu Ile Cys Leu Leu Lys
261       100          105          110
263   Ile Ser Ser Gly Leu Leu Glu Tyr His Ser Tyr Leu Glu Tyr Met Lys
264       115          120          125
266   Asn Asn Leu Lys Asp Asn Lys Lys Asp Lys Ala Arg Val Leu Gln Arg
267       130          135          140
269   Asp Thr Glu Thr Leu Ile His Ile Phe Asn Gln Glu Val Lys Asp Leu
270       145          150          155          160
272   His Lys Ile Val Leu Pro Thr Pro Ile Ser Asn Ala Leu Leu Thr Asp
273       165          170          175
275   Lys Leu Glu Ser Gln Lys Glu Trp Leu Arg Thr Lys Thr Ile Gln Phe
276       180          185          190
278   Ile Leu Lys Ser Leu Glu Glu Phe Leu Lys Val Thr Leu Arg Ser Thr
279       195          200          205
281   Arg Gln Thr
282       210

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VERIFICATION SUMMARY

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